

Application No. 09/823,649

Appendix B

(4 pages)

Get Nucleotide sequences for Site search Database
Map EBI
Queries

Home About EBI Contact Us Publications Services Tools Databases Documentation FTP site Protein of the month

InterPro

InterPro home	Text Search	Sequence Search	Databases	Documentation	FTP site	Protein of the month
Search: <input type="text"/>				Search Entries	<input type="text"/>	<input type="text"/>

Simple | Full HTML Version
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InterPro Protein matches

Select:	Protein accession(s)	<input checked="" type="checkbox"/>	P00582
Refine:	Proteins with alternative splicing:	<input type="checkbox"/>	
	Proteins with known structure:	<input type="checkbox"/>	
	Taxonomy - NCBI tax ID(s):		
Display:	Detailed	<input checked="" type="checkbox"/>	
Sort:	Accession	<input checked="" type="checkbox"/>	

Taxonomy Lineage

no rank: Root node of taxonomy 1
no rank:
cellular organisms 1

Protein Match data

DNA polymerase I (EC 2.7.7.7) (POL I)

- [Table of Matches](#)
- [GO annotation](#)
- [View protein UniProt information](#)



IPR001098	IPR001098	IPR001098	IPR002298	IPR002298	IPR002421	IPR002421	IPR002421	IPR002562	IPR002562	IPR003583	IPR008918
PF00476	PS00447	SM00482	PR00868	TIGR00593	PF01367	PF02739	SM00475	SM00474	SM00278	SM00279	SS1
			655-677 T								
			678-693 T								
			700-723 T								
			730-743 T								
547-927 T	754-773 T	686-892 T	754-779 T	9-928 T	171-277 T	7-169 T	7-268 T	330-517 T	188-207 T	173-208 T	179
			791-802 T								
			813-824 T								
			845-861 T								
			875-888 T								
InterPro Signatures											
IPR001098	PF00476										
IPR001098	PS00447										
IPR001098	SM00482										
IPR002298	PR00868										
IPR002298	TIGR00593										
IPR002421	PF01367										
IPR002421	PF02739										
IPR002421	SM00475										
IPR002562	PF01612										
IPR002562	SM00474										

UniProt :

P00582

Scale:10aa

DPO1_ECOLI

Structure:

GO:




Escherichia coli

IPR003583	SM00278	
IPR008918	SM00279	
IPR008918	SSF47807	
IPR012337	SSF53098	
Structural features		
1dpl	1dpl	
1.10.150.20.17	2kna4	
1.20.1060.10.1	2kna2	
3.30.420.10.16	2kna1	
3.30.70.370.1	2kna3	
c.55.3.5	d2kna1	
e8.1.1	d2kna2	
Structural predictions		
MB_P00582		

ModBase	
PRINTS	
Plam	
PROSITE pattern	
SMART	
SuperFamily	
PDB Chain	

Match Status key:	
T	True

CATH Domain		F False
TIGRFAMs		P Partial
SCOP Domain		U Unknown
		N False negative

IPR001098	DNA-directed DNA polymerase	
IPR002421	5'-3' exonuclease	
IPR002562	3'-5' exonuclease	

InterPro 12.1 Please contact EBI Support with any problems or suggestions regarding this site.
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